

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/872,364

DATE: 10/09/2001

TIME: 09:52:49

Input Set : A:\3759-0107P.ST25 .txt

Output Set: N:\CRF3\10092001\I872364.raw

3 <110> APPLICANT: Ole THRASTRUP et al.  
 5 <120> TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS  
 7 <130> FILE REFERENCE: 3759-0107P  
 9 <140> CURRENT APPLICATION NUMBER: US 09/872,364  
 C--> 10 <141> CURRENT FILING DATE: 2001-06-06  
 12 <160> NUMBER OF SEQ ID NOS: 23  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 36  
 18 <212> TYPE: DNA  
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 71 <210> SEQ ID NO: 7  
 72 <211> LENGTH: 48  
 73 <212> TYPE: DNA

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147 &lt;220&gt; FEATURE:

148 &lt;221&gt; NAME/KEY: CDS

149 &lt;222&gt; LOCATION: (8)..(721)

150 &lt;223&gt; OTHER INFORMATION:

152 &lt;400&gt; SEQUENCE: 15

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157 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
158 15          20          25          30
159 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt      145
160 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
161      35          40          45
162 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act      193
163 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
164      50          55          60
165 act ctc tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg      241
166 Thr Leu Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
167      65          70          75
168 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag      289
169 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
170      80          85          90
171 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct      337
172 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
173 95          100          105          110
174 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa      385
175 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
176      115          120          125
177 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa      433
178 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
179      130          135          140
180 tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag      481
181 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
182      145          150          155
183 aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga      529
184 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
185      160          165          170
186 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat      577
187 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
188 175          180          185          190
189 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc      625
190 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
191      195          200          205
192 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag      673
193 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
194      210          215          220
195 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa      721
196 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

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212 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
213          35          40          45
214 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
215          50          55          60
216 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
217 65          70          75          80
218 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
219          85          90          95
220 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
221          100         105         110
222 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
223          115         120         125
224 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
225          130         135         140
226 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
227 145         150         155         160
228 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
229          165         170         175
230 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
231          180         185         190
232 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
233          195         200         205
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235          210         215         220
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764

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255 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt      97
256 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
257 15          20          25          30
258 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt      145
259 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
260          35          40          45
261 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act      193
262 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
263          50          55          60
264 act ctc tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg      241
265 Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
266          65          70          75
267 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag      289
268 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
269          80          85          90
270 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct      337
271 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
272 95          100          105          110
273 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa      385
274 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
275          115          120          125
276 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa      433
277 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
278          130          135          140
279 tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag      481
280 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
281          145          150          155
282 aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga      529
283 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
284          160          165          170
285 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat      577
286 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
287 175          180          185          190
288 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc      625
289 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
290          195          200          205
291 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag      673
292 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
293          210          215          220
294 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa      721
295 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
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VERIFICATION SUMMARY

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